

5' NNC TGT AAT AGG AGC AGT ATA GGG AAA CCT GGT ACC CTG CAG GTA CTG GTC CGG

AGT TCC TGG GTC GAC CCA CGC GTC CGG CTT TCT GTA GCT GTA ACA TTG GTG GCC

ACA CAC CTC CTT ACA AAG CAA CTA GAA CCT GCG GCA TAC ATT GGA GAG ATT TTT

TTA ATT TTC TGG ACA TGA AGT AAA TTT AGA GTG CTT TCT AAT TTC AGG TAG AAG

ACA TGT CCA CCT TCT GAT TAT TTT TGG AGA ACA TTT TGA TTT TTT TCA TCT CTC

TCT CCC CAC CCC TAA GAT TGT GCA AAA AAA GCG TAC CTT GCC TAA TTG AAA TAA

TTT CAT TGG ATT TTG ATC AGA ACT GAT TAT TTG GTT TTC TGT GTG AAG TTT TGA

GGT TTC AAA CTT TCC TTC TGG AGA ATG CCT TTT GAA ACA ATT TTC TCT AGC TGC

CTG ATG TCA ACT GCT TAG TAA TCA GTG GAT ATT GAA ATA TTC AAA ATG TAC AGA

M Y R

GAG TGG GTA GTG GTG AAT GTT TTC ATG ATG TTG TAC GTC CAG CTG GTG CAG GGC

E W V V V N V F M M L Y V Q L V Q G

TCC AGT AAT GAA CAT GGA CCA GTG AAG CGA TCA TCT CAG TCC ACA TTG GAA CGA

S S N E H G P V K R S S Q S T L E R

TCT GAA CAG CAG ATC AGG GCT GCT TCT AGT TTG GAG GAA CTA CTT CGA ATT ACT

S E Q Q I R A A S S L E E L L R I T

CAC TCT GAG GAC TGG AAG CTG TGG AGA TGC AGG CTG AGG CTC AAA AGT TTT ACC

H S E D W K L W R C R L R L K S F T

AGT ATG GAC TCT CGC TCA GCA TCC CAT CGG TCC ACT AGG TTT GCG GCA ACT TTC

S M D S R S A S H R S T R F A A T F

TAT GAC ATT GAA ACA CTA AAA GTT ATA GAT GAA GAA TGG CAA AGA ACT CAG TGC

Y D I E T L K V I D E E W Q R T Q C

FIGURE 1A

819	828	837	846	855	864
AGC CCT AGA GAA ACG TGC GTG GAG GTG GCC AGT GAG CTG GGG AAG AGT ACC AAC					
S P R E T C V E V A S E L G K S T N					
873	882	891	900	909	918
ACA TTC TTC AAG CCC CCT TGT GTG AAC GTG TTC CGA TGT GGT GGC TGT TGC AAT					
T F F K P P C V N V F R C G G C C N					
927	936	945	954	963	972
GAA GAG AGC CTT ATC TGT ATG AAC ACC AGC ACC TCG TAC ATT TCC AAA CAG CTC					
E E S L I C M N T S T S Y I S K Q L					
981	990	999	1008	1017	1026
TTT GAG ATA TCA GTG CCT TTG ACA TCA GTA CCT GAA TTA GTG CCT GTT AAA GTT					
F E I S V P L T S V P E L V P V K V					
1035	1044	1053	1062	1071	1080
GCC AAT CAT ACA GGT TGT AAG TGC TTG CCA ACA GCC CCC CGC CAT CCA TAC TCA					
A N H T G C K C L P T A P R H P Y S					
1089	1098	1107	1116	1125	1134
ATT ATC AGA AGA TCC ATC CAG ATC CCT GAA GAA GAT CGC TGT TCC CAT TCC AAG					
I I R R S I Q I P E E D R C S H S K					
1143	1152	1161	1170	1179	1188
AAA CTC TGT CCT ATT GAC ATG CTA TGG GAT AGC AAC AAA TGT AAA TGT GTT TTG					
K L C P I D M L W D S N K C K C V L					
1197	1206	1215	1224	1233	1242
CAG GAG GAA AAT CCA CTT GCT GGA ACA GAA GAC CAC TCT CAT CTC CAG GAA CCA					
Q E E N P L A G T E D H S H L Q E P					
1251	1260	1269	1278	1287	1296
GCT CTC TGT GGG CCA CAC ATG ATG TTT GAC GAA GAT CGT TGC GAG TGT GTC TGT					
A L C G P H M M F D E D R C E C V C					
1305	1314	1323	1332		
AAA ACA CCA TGT CCC AAG ATC TAA TCC AGC ACC CCA AAA AAT G 3'					
K T P C P K I * S S T P K N					

FIGURE 1B

1 MYREWVVNVFM - - - MLYVQLVQGSSNEHGPVKRSSQST 873352
 1 MH - - - LLGFFSVACSLLAALLPGPPEAPAAA - AFESG GI 1150989

37 LERS - - - - - EQQIRAAASSLEELLRITHS 873352
 36 LDLS DAEPDAGEATAYASKDLEQLRISVSSVDELMTVLYP GI 1150989

60 EDWKLWRCRLRLKSE - - - - - TSMDSRSAASHRSTRF AATF 873352
 76 EYWKMYKCLQLRKGGWQHNRREQANLSR - - T EETIKFAAAH GI 1150989

94 YDIETLKVIDEEWQRTQCCSPRETCEVEVASELGKSTNTTFFK 873352
 114 YNTEILKSIDNEWRKTQCMPREVCI DVGKEFGVATNTTFFK GI 1150989

134 PPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 873352
 154 PPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLS GI 1150989

174 SVPELVVPVKVANHTGCKCLPTAP - - RHYPYSIIRRSIQIPE 873352
 194 QGPKPV TISFANHTSCRCMSKLDVYRQVHSIIRRS LP - AT GI 1150989

212 EDRCSHKKLCPI DMLWDSNKKCKV LQEEENPLAGTED - - - 873352
 233 LPQCQAANKTCPTN YMWNNHHICRC LAQEDFMFSSDAGDDS GI 1150989

249 - - - - - HSHLOE - - - - - - - - - 873352
 273 TDGFHDI CGPNKELDEETCQCVCRAGLRPA SCGPHKELDR GI 1150989

255 - - - - - - - PALCGPHMMFDEDRCECVCKTPCPK - - - 873352
 313 NSCQCVCCKNKLFFSQCGANREFDENTCQCVCCKRTCP RNQP GI 1150989

280 - - - - - - - - - - - - - - - - - - - 873352
 353 LNP GKACECTESPQKCLLKGGKFFHHQTCS CYRRPCTNRQ GI 1150989

280 - - - - - - - - - - - - - - - - - - - 873352
 393 KACEPGFSYSEEVCRVPSYWKRPQMS GI 1150989

FIGURE 2

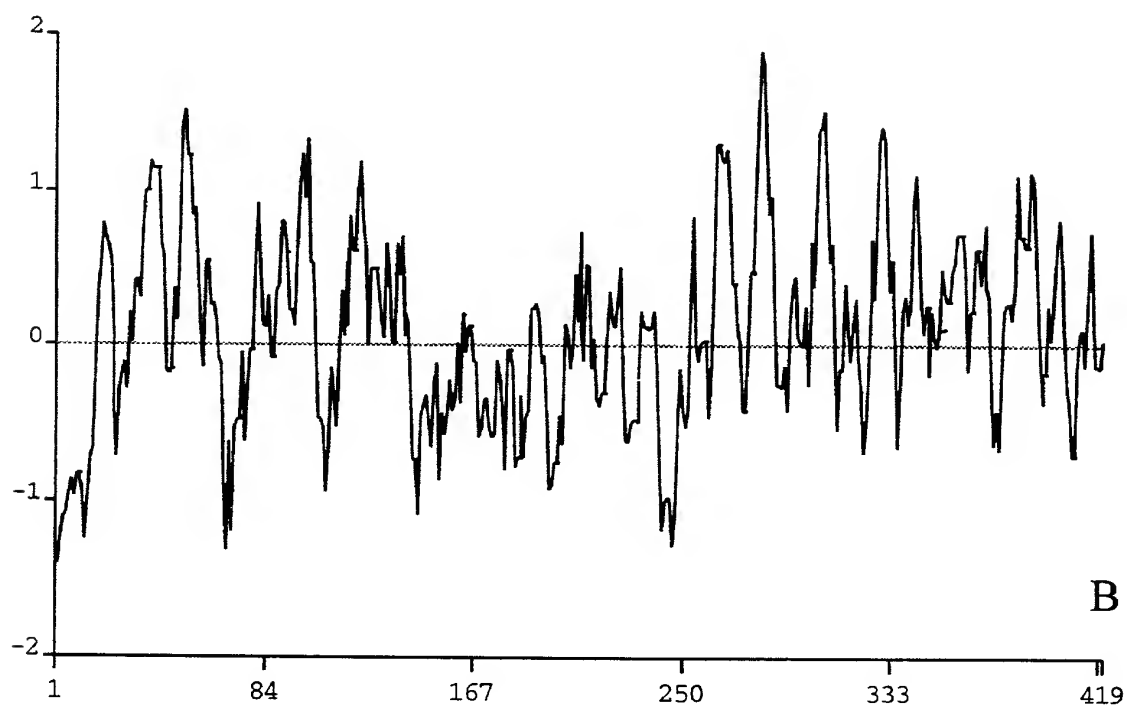
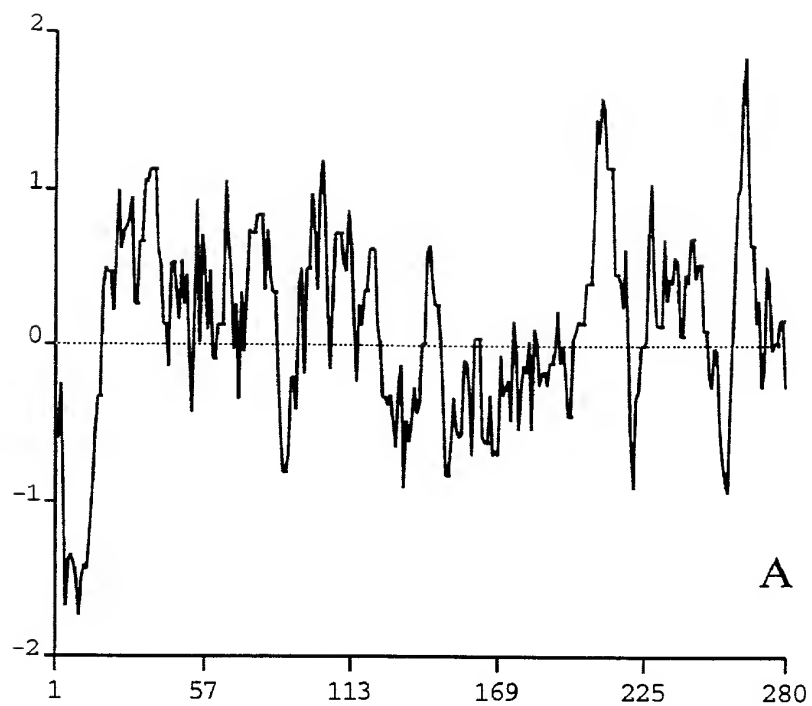


FIGURE 3